

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 14:29:52 : Search time 7114.74 Seconds
(without alignments)
5809.054 Million cell updates/sec

Title: US-09-052-089a-8
Perfect score: 1975
Sequence: 1 GGCACGAGGTGGTGGAGC.....CAAAAAAAAAAAAAAAAAAAAA 1975

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :
1: Gendbml:*
2: gb_ba:*
3: gb_htg:*
4: gb_in:*
5: gb_om:*
6: gb_ov:*
7: gb_pat:*
8: gb_ph:*
9: gb_pl:*
10: gb_pr:*
11: gb_ro:*
12: gb_sts:*
13: gb_sy:*
14: gb_un:*
15: gb_vi:*
16: em_ba:*
17: em_fun:*
18: em_hum:*
19: em_in:*
20: em_mu:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_un:*
30: em_vi:*
31: em_htg_hum:*
32: em_htg_inv:*
33: em_htg_other:*
34: em_htg_inv:*
35: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query 8
No. Score Match Length DB ID Description

1	1952	98.8	1981	10	MMU77844	U77844 Mus musculi
2	1880	95.2	2024	10	BC017374	BC017374 Mus muscu
3	1075.4	54.5	2065	6	AR072729	AR072729 Sequence
4	1075.4	54.5	2065	6	BD006990	BD006990 Modulator
5	1072.2	54.3	2002	9	BC019283	BC019283 Homo sapi
6	1072.2	54.3	2010	9	BC000310	BC000310 Homo sapi
7	1062.8	53.8	2007	9	HSU77845	U77845 Human hTRIP
8	952.6	48.2	3694	10	BC006929	BC006929 Mus muscu
9	111.4	5.6	7542	6	AX350344	AX350344 Sequence
10	111.4	5.6	163424	2	AC099330	AC099330 Homo sapi
11	108.2	5.5	129747	9	HS465N24	AL031432 Human DNA
12	101.8	5.2	110000	2	AL353694_2	Continuation (3 of
13	101.8	5.2	163424	2	AC099330	AC099330 Homo sapi
14	72.4	3.7	39410	5	FR165K09	AF010317 Fugu rubr
15	64	3.2	7218	6	166494	166494 Sequence 14
16	57.6	2.9	2065	14	AF410847	AF410847 Ovine her
17	55.2	2.8	203984	2	AC067854	AC067854 Homo sapi
18	54.2	2.7	110000	2	LMFICHR34_16	Continuation (17 o
19	53.8	2.7	207683	2	AC098712	AC098712 Mus muscu
20	53.2	2.7	216191	2	AC090495	AC090495 Mus muscu
21	51.6	2.6	3127	14	AF305694	AF305694 Kaposi's
22	51.4	2.6	211158	2	AC073609	AC073609 Mus muscu
23	51.2	2.6	1683	9	CHPINVOL	M26514 Chimpanzee
24	51.2	2.6	133661	14	U93872	U93872 Kaposi's sa
25	50.8	2.6	219200	10	AL589701	AL589701 Mouse DNA
26	50.4	2.6	3012	14	AF360120	AF360120 Human her
27	50.2	2.5	180385	9	AC007461	AC007461 Homo sapi
28	50	2.5	125020	9	AF429315	AF429315 Homo sapi
29	49.6	2.5	28559	14	AF148805	AF148805 Kaposi's
30	49.2	2.5	140207	2	AC016837	AC016837 Homo sapi
31	49.2	2.5	164310	9	AC019294	AC019294 Homo sapi
32	49.2	2.5	180795	2	AC027104	AC027104 Homo sapi
33	49.2	2.5	227605	2	AC073564	AC073564 Mus muscu
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35	49	2.5	206497	10	AC084389	AC084389 Mus muscu
36	48.8	2.5	2160	10	AY033497	AY033497 Mus muscu
37	48.8	2.5	1993	37	AB033744	AB033744 Mus muscu
38	48.8	2.5	5894	3	ACMHC	Y00624 Acanthamoeb
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41	47.2	2.4	35848	2	AC011553	AC011553 Homo sapi
42	47	2.4	172148	3	LMFP696	AL512293 Leishman
43	47	2.4	175463	2	AC095873	AC095873 Rattus no
44	47	2.4	199508	2	AC098555	AC098555 Rattus no
45	46.8	2.4	2931	14	AF192756	AF192756 Kaposi's

ALIGNMENTS

RESULT 1
LOCUS MMU77844 1981 bp mRNA linear ROD 25-APR-1997
DEFINITION Mus musculus mTRIP (mTRIP) mRNA, complete cds.
ACCESSION U77844
VERSION U77844.1 GI:2039305
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1981)
AUTHORS Lee,S.Y., Lee,S.Y. and Choi,Y.
TITLE TRAF-interacting protein (TRIP): a novel component of the tumor
necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
that inhibits TRAF2-mediated NF-kappaB activation
JOURNAL J. Exp. Med. 185 (7), 1275-1285 (1997)
MEDLINE 97258620
REFERENCE 2 (bases 1 to 1981)
AUTHORS Lee,S.Y., Lee,S.Y. and Choi,Y.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1996) Immunology, The Rockefeller University,
1230 York Avenue Box 295, New York, NY 10021, USA

FEATURES
source location/Qualifiers
1. .1981
/organism="Mus musculus"
/db_xref="taxon:10090"
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/product="mfr1p"
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/db_xref="GI:2039306"
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CKKMTMEIILLOSSEVEEMIRDMGVGOSAEOLAYVCVSLKREYENLKERRAT
GELADRIKDLVSRSLKLTINLELDKLEBSAOKDLOSADDETISLKKLMIIDG
TSLPPTNETVSLVESPAPVEMNPRHLHOPPEGDEIDLTNTFEDVNTPTOTSGQ
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AVLGOKQPNRTAESRSSTDVVRIGFDLGRRTKFIQPRDTITIRPVPKSKAKSKOK
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BASE COUNT 532 a 489 c 534 g 426 t
ORIGIN

Query Match 98.8%; Score 1952; DB 10; Length 1981;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 GGCACGAGTGGTGGGAGGCAAAATTTGAAGAACCGGAGCGGTGGCCGTTCCACCAA 60
Db 7 GGCACGAGTGGTGGGAGGCAAAATTTGAAGAACCGGAGCGGTGGCCGTTCCACCAA 66
Qy 61 CTGTGTCTGTCTGTGGAGCTGTTCCCTGGCTGCTGAGTCGAGCCATCATGCTATC 120
Db 67 CTGTGTCTGTCTGTGGAGCTGTTCCCTGGCTGCTGAGTCGAGCCATCATGCTATC 126
Qy 121 CTGTCTGTCTGTCTGTGGAGCTGTTCCCTGGCTGCTGAGTCGAGCCATCATGCTATC 180
Db 127 CTGTCTGTCTGTCTGTGGAGCTGTTCCCTGGCTGCTGAGTCGAGCCATCATGCTATC 186
Qy 181 CACGTGGCCACACTTTTCACTGCAATGCTAATCCAGTGTGTTGAGACGACCAAGT 240
Db 187 CACGTGGCCACACTTTTCACTGCAATGCTAATCCAGTGTGTTGAGACGACCAAGT 246
Qy 241 CGGACCTGCCACAGTGTAGATCCAGTGTGGCAAAAGACTATTATTAACAACTTTC 300
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Qy 361 GACAGCGTCAAAAGCTCAGCTTCCAGAAAGACAGGGAACCGGAGCGCCACTT 420
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Db 427 ATGCACTCTAGGAGACCTCTGGAAGACGCAATGCTACCGTGGATGCCCTACAGAC 486
Qy 481 GCCCTTAACAAGCAGAGATCTGTGTCCACCTGAAAAAAGATGAATTTCTCTGAG 540
Db 487 GCCCTTAACAAGCAGAGATCTGTGTCCACCTGAAAAAAGATGAATTTCTCTGAG 546
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Db 547 CAGCGGAGAGTGAACCAAAAGCTCGGAGAGAGCGCCACGACTCAATGCAAGATG 606
Qy 601 AAACCATGAGCAAAATTTGAGCTCTCTACTCCAGAGCCAGCTTCTGAGGTGAGAGATG 660
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Db 727 CTCAAGAAAGAGTATGAGAAATCTGAAGAGAGCTGGAAAGCCACAGGGAAGTGGCTGAC 786
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Db 1146 GGAGAGGAGCAGCTCTCCATGCAAGATGTCTCAAGAGGTGACAAAGCTTCAAGCC 1205
Qy 1200 GGAATCCAGCTCTCACTGGGTGACAGAGATGTGTAGAGAGCTAGATGAGAACTGCG 1259
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Qy 1680 TGACCACTTTACGTGTCGAGTCAAGCAGAGGCTACTTCCAGTGTGAGGCTTTGCTTATAG 1739
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Qy 1740 CTACAAACAGGTGTGAGCTCTCTTGTGTTTATAGAAACAGGTCACATTTGACTCTA 1799

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Db 1746 CTACAACGAGTGTGGCTGACTCTTTGTTTATTAGAAACAGGTCACATGACTCTA 1805
QY 1800 AGGAGGAGGAGGCTGAGAGATCTTATGACGCTGAGAGACCTGGCTTGAACCTCTG 1859
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QY 1860 CTTGCCCTCAGCTTATGCTTGAATATGAGGAGTGTGATAGGAAAGTTGGG 1919
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QY 1920 AAGTTTCTGTGTAAATAAAGGATCTTTCTCAAAAAA 1975
Db 1926 AAGTTTCTGTGTAAATAAAGGATCTTTCTCAAAAAA 1981
RESULT 2
BC017374 2024 bp mRNA linear ROD 14-NOV-2001
LOCUS Mus musculus, TRAF-interacting protein, clone MGC:13919
DEFINITION IMAGE:3990371, mRNA, complete cds.
ACCESSION BC017374 GI:16924208
VERSION BC017374.1
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2024)
REFERENCE Strausberg, R.
AUTHORS Direct Submission
TITLE Submitted (13-NOV-2001) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAC Plate: 18 Row: d Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6755868.
FEATURES
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1. 2024
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Query Match 95.2%; Score 1880; DB 10; Length 2024;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1935; Conservative 0; Mismatches 15; Indels 6; Gaps 4;
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Db 11 ATTTGAAGGAACCGGAGCGCGGCGGTGGCCACCAAACTGTCTGTGCGTGGCAGC 70
QY 81 TGGTTCCCTGGGCGTCTTGAAGTGAAGCCATCATGCTTCCTCTGTGACATCTG 140
Db 71 TGGTTCCCTGGGCGTCTTGAAGTGAAGCCATCATGCTTCCTGTGACATCTG 130
QY 141 CTCGACTTCTTGATGATCTCCGCTGAGCTGCTGCCATCCTACTGTGGCCACTTTTCA 200
Db 131 CTCGACTTCTTGATGATCTCCGCTGAGCTGCTGCCATCCTACTGTGGCCACTTTTCA 190
QY 201 TCTGCATGCTAATCCAGTGTGTTGAGACAGACCAAGCGGAGCCGTCACAGTGTAG 260
Db 191 TCTGCATGCTAATCCAGTGTGTTGAGACAGACCAAGCGGAGCCGTCACAGTGTAG 250
QY 261 AATCCAGTTGGCAAAAGACTATTATTAACAACTTTCTTGACCTCCGCCAGAGA 320
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QY 321 GGAAGATGCTTGGAGTCAAGATTTCTTAAGATGAAGTGAAGCTCAAGCTCAGCT 380
Db 311 GGAAGATGCTTGGAGTCAAGATTTCTTAAGATGAAGTGAAGCTCAAGCTCAGCT 370
QY 381 TTCCCAAGAAAGACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 440
Db 371 TTCCCAAGAAAGACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 430
QY 441 CTTGGAAGAAAGCAATGCTACCGTGGAGTCCCTACAGAACGCTTAAACAAGGAGAGAT 500
Db 431 CTTGGAAGAAAGCAATGCTACCGTGGAGTCCCTACAGAACGCTTAAACAAGGAGAGAT 490
QY 501 GCTGTGTTCCACCTGTAAGAAACAGATGAAGTCTTGAGACAGGAGGAGATGACCAA 560
Db 491 GCTGTGTTCCACCTGTAAGAAACAGATGAAGTCTTGAGACAGGAGGAGATGACCAA 550
QY 561 ACAAGCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 620
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Db 611 GCTCTCACTCCAGAGCCAGGCTTCTGAGTGAAGGAGATGATTCGAGACATCTGGGTGGG 670
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QY 741 TCTGAAGAGAGCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 800
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Db 851 GAGGTCAAGCCAGAGAGACTTACAAGTGTGACACAGAGATACAGAGCTTAAGAAAGAA 910

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QY	980	GCTCTGGTTTTTGAGAGGCCACGCCCCCTTGAGATGTAGTAACCCGAGGCTTTCACACAGCCAC	1033
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QY	1040	CCTTGGTGATGAGATTGATCTCAATACACCTTTGATGTAAATACCCTTCCACCCAGA	1099
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QY	1100	CCTTGGCTCCAGACATTTGCCCTCCCAAGAAAGTGCGCTGGAGAGGACGCTGTCCCA	1155
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QY	1340	GCACAGATGTGTAGAAATAGGCTTTGATGGGCTTGAGAGACGACAAAATTCATCCAGC	1399
Db	1330	GCACAGATGTGTAGAAATAGGCTTTGATGGGCTTGAGAGACGACAAAATTCATCCAGC	1389
QY	1400	CTAGGACACAAACCATTAATCCGACACAGTGGCTCTTAAATGTCAGAGGCCAAGAGTAAACAGA	1455
Db	1390	CTAGGACACAAACCATTAATCCGACACAGTGGCTCTTAAATGTCAGAGGCCAAGAGTAAACAGA	1444
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QY	1520	AGTAAAGGTCACCAAGATGATGTTTGCATTAAGTGGGCCAAGACTGGCTTAACCGGAAG	1579
Db	1510	AGTAAAGGTCACCAAGATGATGTTTGCATTAAGTGGGCCAAGACTGGCTTAACCGGAAG	1566
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Db	1570	TGTTTTTGAGATGAGCTCCTCTTGACACAGTCCCAAGAGATGCCACAGAAAACACTT	1622
QY	1640	CCTGTGTCACTGCGCCCTGCACACACTGGAGAGCCACATGCACAGTTTACTGTTCCGA	1699
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QY	1700	TCAGAGGGCCTACTTCCAGTGTGAGGCTTTTCTTAAGCTCAACCAAGGTCGGCTGG	1759
Db	1690	TCAGAGGGCCTACTTCCAGTGTGAGGCTTTTCTTAAGCTCAACCAAGGTCGGCTGG	1748
QY	1760	ACTCCTTTGTTTTATATAGAACAGGGTCACATTTAGCTTAAGTGAATGGAGTGGCTGGAG	1819
Db	1750	ACTCCTTTGTTTTATATAGAACAGGGTCACATTTAGCTTAAGTGAATGGAGTGGCTGGAG	1809
QY	1820	GATCCTATGCAAGGCTGGAGAACCTGGGCTTGAACCTCTGCTGGCTCCAGCTTATGGCT	1879
Db	1810	GATCCTATGCAAGGCTGGAGAACCTGGGCTTGAACCTCTGCTGGCTCCAGCTTATGGCT	1866
QY	1880	TGAATTTTGAGGCTGAGGTGTATAGGAAGAGTTGGGAAGTTTCTGTATAAATAA	1933
Db	1870	TGAATTTTGAGGCTGAGGTGTATAGGAAGAGTTGGGAAGTTTCTGTATAAATAA	1928
QY	1940	AAAGGATCTTTCTTCAAAAAAAAAAAAAAAAAAAAAA	1975
Db	1939	AAAGGATCTTTCTTCAAAAAAAAAAAAAAAAAAAAAA	1964

[illegible]

OY	801	GTTCCTTAGAGACGAAGTTGAAGACCTCTCCAAACACTGAGCTGGATATCGGCAAGTTAAGAACT	860
Db	792	TTCTCTCCAGAAGCAAGTTGCGACAGCTCTACCTCTCTGTATTTGGATCGAGGCCAAGTTAAGAACT	851
OY	861	GAGGTCAAGCCAGCAAGAACTTACAAAGTCTGTACCAGAGATCACAGAGCTTAAGAAAGA	920
Db	852	GAAGTCAGCCCAAGAGAACTTACAGAGTGTGTGACAAAGAAATCATAGAGCTTGAAGAAAGA	911
OY	921	GTCCTGATGATCTTCAGAGGAACCTTGAGCCCTGCCTCC - GCGAACCAATGAGAGGCTCAGCC	979
Db	912	G-CTAAGAGATGTCTGACAGAAACCTTGAACTGTGCACAGTGGCCAGTGGACTGTGCAC	970
OY	980	GCCCTGTTTTTGAGAGGCCCGCCCTGTGTGAGATGATGACCCGAGGCTTACACAGCCAC	1039
Db	971	GCCCTGTTTTTGAAGAGAGCCCGCCCTGTGTGA - - GGTGAAATCTGAAGATCTCGCGCGGGCAT	1027
OY	1040	CCCTTGGGTAATGAGATTGATCTCAATACCAACCTTTGATGTAAATACCCCTCCACCCGA	1099
Db	1028	CCCTTCCGTAATGATATTGATCTCAATGCTAACCTTTGATGTGATCTCTCCCGAGCCGGC	1087
OY	1100	CCCTTGGGCTCCAGCACTTGGCTCTCCCAAGAAGCTGTGCTGTGAGAGGGCAGCCTTCCCA	1159
Db	1088	CCCTCAGCTCCAGCAAGTGTTACTACGAAAACTTTGCCATAGAAATGTCACACTCCCAA	1147
OY	1160	TGCAGAAATGTCTTCAGAGAGGTGCACAAAGTCTCCAGCCGAGTCCAGAGCTTCTCATCGG	1219
Db	1148	TTTCAGGATGTCTCCCAAGAAATATATGCAAAAGGCCCGCCAGAAAGATGCCAGCTCTCATCGG	1207
OY	1220	GTCGCGCAGCGATGTGTGTGAGAGACTGTGATGAGAACTGGCTGTGCTCTCTCTCTCA	1279
Db	1208	GTCGCGCAGAGCTGTGTGAGAGAGCCAGATGAGAACTGATGTGCTCTCTCTCTCTCTTTTGG	1267
OY	1280	TCCCGAATGTGCTGTCTGGGTCAAAACAGCCCAACAGAGCCACACAGATATCCCGAACA	1339
Db	1268	TCCGGAATGTGCATCTCTAGGCGCAAAACAGCCCAAGAGGCCAGGTCTAGAGTCTCTTGTCA	1327
OY	1340	GCACAGATGTGTGTAGAAATAGCTTTGATGTGGCTTGTGAGAGCAAAATTCATCCAGC	1399
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OY	1400	CTAAGGACACAAACCATTAATCCGACAGGTGCTGTTAATGTCACAAAGGCCAAAGATTAACGA	1459
Db	1388	CTACTGACACAGTATATGATCCGCCATATGCTGTTAAGGCCAAAGAGTAAGCGAGA	1447
OY	1460	AAGTGAATTAAGAGTGTGATGTTCTGACCTCCAGGCCCAAGTGTGATACCTTCTTAATGC	1519
Db	1448	GGGTGAGGTGTAAAGACAGTGTCTTCTCTTCCAGGCCAAGCTGTGACACACTTCTGTGTGT	1507
OY	1520	AG-----TGAAGCGTGAACCAAGATGTGTTTCAATTAATGTGGGCCAAGAC	1564
Db	1508	CGTGAGAAACAGTGTGATCTGACCAATAGGCCAGACACATCTGCTGCTCAACTGTAGTCAAGÄ	1567
OY	1565	CTGCGTAAACCGGAAGTCTTTTGTGAAGATGTGCTCTCTTGTGAGC-----	1608
Db	1568	CTGTCCAGGAGGGGTTTTTGTGTGACAGAGGCCCACTTTTGGGACCAAGCCTGAGGTGAAG	1627
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Db	1628	GGCAGACAAACAGGTGTGAGGGTGTGATGTGACACCCAGAGACTGTCTTCTGCTCCACACC	1687
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Db	1688	TGCCCACTCTTCAATGATGTGGAGCTGACATGACAGCCACATGATCTGTGTGAGCGTCC	1747
OY	1711	TACTTTCAGTTGCAAGGTTTTTGTCTTAATGTACACACAGTGTGGCTGTGACTCTTTGT	1770
Db	1748	TGCTCTCTGTGTCCAGGCTCTCTGTTTTATATGCAATGATCAATGTGTGCAACACTTTTGG	1807
OY	1771	TTTATATGAACAGGCTGACATATGATCTTAAGTGGATGGAGTGTGAGAGATCTATCA	1830
Db	1808	GCTCTGAGACACGAGTACTTGTGTGACTGTCTGTGTGACAG-----AGTCTTGAAGC	1862
OY	1831	GCTGTGAGGACCTGTGAACTCTGTGCTGCTCCAGCTTAATGTCTTGAATTAATGG	1890

Db	1863	ATCTAGGCAGCCTTAGCCCAAGCTTCTTACCTGCCCTTGACTTGCTTGTAGGCATAGCCT	1922
Qy	1891	GCTGAGGTGGTGATAGGGAAGGTGGGAAGTTTCTGTAAATATAAAAAGGATCTT	1950
Db	1923	GGGCCAACAGGGGTGGGGAATGAGATAGCATGATGTATGAGAGAGATGAAGATTT	1982
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LOCUS					
DEFINITION	BD006990	2065 bp	DNA	linear	PAT 31-JAN-2002
ACCESSION	BD006990	Modulators of BRCA1 activity.			
VERSION	BD006990.1	GI:18635361			
KEYWORDS	JP 2001502893-A/1.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 2065)				
AUTHORS	Lublinfeld,B., Porakisu,P., Rigenferuta,C. and Buon,T.T.				
TITLE	Modulators of BRCA1 activity				
JOURNAL	Patent: JP 2001502893-A 1 06-MAR-2001;				
COMMENT	ONIX PHARMACEUTICALS INC				
	OS unidentified				

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FEATURES
PI  BONY LUBINFELD, PAUL PORAKISU, CAROL RIGEMFEREUTA, TETRIRIN T BUON
PC  C12N5/09, A61K38/00, A61P43/00, C07K11/435, C07K16/18, C12N1/15,
PC  C12N1/19,
PC  C12N1/21, C12N5/10, C12P21/02//C12P21/08, C12N15/00, C12N5/00, PC
    A61K37/02
CC  Strandedness: Double;
CC  Topology: Linear;
FH  key          Location/Qualifiers
FT  CDS          103..151.
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Matches 1460; Conservative	0;	Mismatches 426;	Indels 59;	Gaps 7;

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QY	192	CTTGGAGTGGCCATATCTCATGTGGTTTGACAGCACCAAGTGGAGCTGCCACAGTGGCCG	251
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Db	192	CTTGGAGTGGCCATATCTCATGTGGTTTGACAGCACCAAGTGGAGCTGCCACAGTGGCCG	251
QY	261	AATCCAGGTGTGGCAAAAAGACTATTATTAACAAACTTTTGTGACCTGCCGAGGAGA	320
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Db	252	AATCCAGGTGTGGCAAAAAGCAACCATTAATCAATAAGCTCTTTGTATCTTGCCGAGGAGA	311
QY	321	GGAGAAATGCTTTGGATGACGAATTTCTTAAGATATGAATGAACTGACAGCGTCAAAAGTCAAGCT	380
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QY 381 TTCCAGAAAGACAGGAGAAACGGAGACAGCCAGCATTTATCGACACTTACGAGAC 440
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QY 501 GCTGTTTCCACCCGAAAGAAAGATGATGATCTCTGAGAGACGGCGAGATGAGACCA 560
Db 492 GCTGCTCCACACTGAAAGAAAGCAGATGATGATCTCTGAGAGACGGCGAGATGAGACCA 551
QY 561 ACAAGCTCGGAGAGAGGCCACCGACTCAAGTCAAGATGAAAGCAATGAGAGCAATTTGA 620
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QY 631 GCTCTACTCCAGAGCCAGCGTTCTGAGAGTGAAGATGATTCGACATGAGTGTGG 680
Db 612 GCTTCTACTCCAGAGCCAGCGCTCAGAGTGAAGATGATTCGACATGAGTGTGG 671
QY 681 ACAGTCAAGGAGAGAGCTGGCTGTGACTGCTGCTCCCAAGAAAGATATAGAA 740
Db 672 ACAGTCAAGGAGAGAGCTGGCTGTGACTGCTGCTCCCAAGAAAGATATAGAA 731
QY 741 TCTGAGAGACCTCGGAGAGGCCACAGGGAACTGGCTGACAGCTTGAAGAGATTTGT 800
Db 732 TCTAAAGAGAGAGAGAGGCTCAGGGAGTGGCTGACAAAGCTGAGAGAGATTTTGT 791
QY 801 GTCTCTAGAGACAACTGTAAGACTCTCAGACAGTGAAGTGAAGGCAATTTAGAACT 860
Db 792 TTCTCCCGAGAGCAAGTTGACAGAGCTGACTGATGATGATGATGATGATGATGATGAT 851
QY 861 GAGGTCACCCGAGAGAGCTTACAAAGTGTGACAGAGATGACAGAGATGACAGAGATGACAG 920
Db 852 GAGGTCACCCGAGAGAGCTTACAAAGTGTGACAGAGATGACAGAGATGACAGAGATGACAG 911
QY 921 GTCTGATGATCTCGAGAGAACCTTGAAGCTGCTGCTC -GCGACCAATGAGAGAGCTGAC 979
Db 912 G-CTAGAGATGCTGAGAGAACTTGAAGCTGCTGACAGCTGAGAGAGAGAGAGAGAGAGAG 970
QY 980 GCTGCTTTTGAAGAGCCAGCCCTGTGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 1039
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QY 1040 CCTTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
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QY 1100 CCTTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1159
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Db 1568 CTGTCCAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1627
QY 1609 -----AGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1652
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Db 1688 TGCCCACTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1747
QY 1711 TACTTCCAGTTCAGAGAGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1770
Db 1748 TGCTCTGTTCCAGAGAGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1807
QY 1771 TTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1830
Db 1808 GCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1862
QY 1831 GCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1890
Db 1863 ATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1922
QY 1891 GGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1950
Db 1923 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1982
QY 1951 TTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1975
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RESULT 5
 BC019283
 LOCUS
 DEFINITION Homo sapiens, TRAF Interacting protein, clone MGC:3959
 ACCESSION BC019283
 VERSION BC019283.1 GI:17939476
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2002)
 Strausberg, R.
 Direct Submission
 Submitted (13-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Rudin Laboratory
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 BC Cancer Agency, Vancouver, BC, Canada
 info@cgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Leticia Hsiao, Martin Krzyzanski, Reta Kuchel, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline

Db 1613 GGCAGACAAACAGGATGAGTGTGGACACCCAGAGACGCTCTTCTGCTCCACACC 1672
Qy 1653 CGCCCTGACAC-ACATGGGAGACCATATGACCATTTACTGTTCCATCAGCAGGCC 1710
Db 1673 TGCCCCATCTTACAGCTGAGGAGCTGATGATGACGACCCATGATGCTCAGCAGGCC 1732
Qy 1711 TACTTCCAGTTGACAGGTTTGTATATAGTACAAACAGTGTGGCTGGACTCTTTGT 1770
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Qy 1771 TTTTATAGACAGGCTCATTTGACTCTAAGTGTGATGGAGTGTGAGATCTTATGCA 1830
Db 1793 GCTGGAGACACGCTGCTGTTGACTGTCTGTGGACAG-----AGTCTTGAAGC 1847
Qy 1831 GCGTGGAGACCTGCGCTTAACTCCGCTGCTCCAGCTTATGCTTGAATATAGG 1890
Db 1848 ATCTCAGGACCTCAGCCCAAGCTTCTACCTGCTTGAATCTCTTGAAGCATAGCCT 1907
Qy 1891 GGTGAGTGTGATAGGGAAGTGGGGAAGTTTCTGTATAAATTAAGGATCTT 1950
Db 1908 GGGCCAGCAGAGGTGGGTAATGAGAGATGAGATGATGATGAGAGATGGAATTT 1967
Qy 1951 TTCTTCAAAAAAAAAAAAAAAAA 1975
Db 1968 TCATGTAAATTAATTAATTAATTA 1992

RESULT 6
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DEFINITION Homo sapiens, TRAF Interacting protein, clone MGC:8424
IMAGE:2821007, mRNA, complete cds.
ACCESSION BC000310
VERSION BC000310.1 GI:12653088
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2010)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland.
Web site: <http://www.nisc.nih.gov/nisc-mgcdbgri.nih.gov/>
Contact: nisc-mgcdbgri.nih.gov

Shervenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McKloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantilop, S., Thomas, P.J.,
Tjongsom, E.E., Touchman, J.W., Tsurganov, C., Vogt, J.L., Walker, M.A.,
Zhang, L.H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Series: IRAL Plate: 1 Row: e Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5032194,
Location/Qualifiers

FEATURES
source

1. 2010

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Contains two novel genes, ESTs, GSSs and Cpg Islands, complete
sequence.
ACCESSION AL031432
VERSION AL031432.1 GI:4375969
KEYWORDS HTG; Cpg Island.
SOURCE human.
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 129747)
AUTHORS Wilson,S.
JOURNAL Direct Submission
Submitted (11-FEB-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Mar 7, 1999 this sequence version replaced gi:4176479.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 465N24. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu), where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre Chromosome 1
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chrl465N24>
465N24 is from the library RPC13 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see <http://bacpac.med.buffalo.edu/VECTOR:PCYPAC2>.
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9092..9137
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/note="23 copies 2 mer at 100% conserved"
9229..9326
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12833..13130
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13476..14035
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14331..14466
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14467..14600
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14893..15096
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15487..16041
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16069..16773
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16774..17068
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17071..17384
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17385..17451
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17567..17775
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/note="L1ME3A repeat: matches 4012..4208 of consensus"
17912..18219
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18401..18922
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18923..19226
repeat_region
/note="AluSx repeat: matches 1..304 of consensus"

Insert size: 162724; sum-of-contigs
Quality coverage: 9.0x in Q20 bases; agarose-fp
Quality coverage: 11.2x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 4608: contig of 4608 bp in length
* 4609 4708: gap of unknown length
* 4709 10289: contig of 5581 bp in length
* 10290 10389: gap of unknown length
* 10390 17105: contig of 6716 bp in length
* 17106 17205: gap of unknown length
* 17206 45100: contig of 27895 bp in length
* 45101 45200: gap of unknown length
* 45201 65174: contig of 19974 bp in length
* 65175 65274: gap of unknown length
* 65275 90719: contig of 25445 bp in length
* 90720 90819: gap of unknown length
* 90820 119377: contig of 28558 bp in length
* 119378 119477: gap of unknown length
* 119478 163424: contig of 43947 bp in length.

FEATURES

source

Location/Qualifiers

1. 163424

/organism="Homo sapiens"

/db_xref="taxon:9606"

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/clone-lib="RP11-78010"

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/note="assembly_name:Contig74"

misc_feature

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BASE COUNT 40950 a 40937 c 39779 g 40912 t 846 others

ORIGIN

Query Match

Best Local Similarity 93.8%; Score 101.8; DB 2; Length 163424;

Matches 106; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 616 ATTGAGCTCTACTCCAGAGCCAGCTTCTGAGGTGAGAGATGATTCGAGACATGGGT 675

Db 55015 ATTGAGCTTCTACTCCAGAGCCAGCTTCTGAGGTGAGAGATGATTCGAGACATGGGT 54956

OY 676 GTGGAGACAGCAGCGGTGAGAGCAGCTGCTGCTACTGCTGCTCCCAAGAA 728

Db 54955 GTGGAGACAGCAGCGGTGAGAGCAGCTGCTGCTACTGCTGCTCCCAAGAA 54903

RESULT 14

FR165K09/c

LOCUS FR165K09 39410 bp DNA linear VRT 23-JAN-2002

DEFINITION Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.

ACCESSION AJ010317.1 GI:3928163

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

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JOURNAL

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PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

GRM7 gene; metabotropic glutamate receptor 7; plasminogen related growth factor receptor 3; PRGFR3 gene; Sand gene; TRAF interacting protein; trip gene.

Takifugu rubripes

Takifugu rubripes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

1 (sites)

Cottage,A., Clark,M., Hawker,K., Umrantia,Y., Wheller,D., Bishop,M. and Elgar,G.

Three receptor genes for plasminogen related growth factors in the genome of the puffer fish Fugu rubripes

FEBS Lett. 443 (3), 370-374 (1999)

99148833

10025966

2 (sites)

Cottage,A.J., Edwards,Y.J. and Elgar,G.

SAND, a new protein family: from nucleic acid to protein structure and function prediction

Compar. Funct. Genom. 2, 226-235 (2001)

3 (bases 1 to 39410)

Cottage,A.J.

Direct Submission

Submitted (15-AUG-1998) Cottage A.J., HGMPRC, Computing, Hinxton, Cambridge, CB10 1SB, UK

Location/Qualifiers

1. 39410

/organism="Takifugu rubripes"

/db_xref="taxon:31033"

/clone="cosmid 165K09"

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Intron	complement(7291. .7383) /gene="TRIP" /number=7
exon	complement(7382. .7495) /gene="TRIP" /number=7
Intron	complement(7494. .7644) /gene="TRIP" /number=6
exon	complement(7643. .7737) /gene="TRIP" /number=6
Intron	complement(7736. .7817) /gene="TRIP" /number=5
exon	complement(7816. .7943) /gene="TRIP" /number=5
Intron	complement(7942. .8030) /gene="TRIP" /number=4
exon	complement(8029. .8068) /gene="TRIP" /number=4
Intron	complement(8067. .8195) /gene="TRIP" /number=3
exon	complement(8194. .8277) /gene="TRIP" /number=3
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exon	complement(8358. .8415) /gene="TRIP" /number=2
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exon	complement(8496. .>8593) /gene="TRIP" /number=1
exon	<9737. .9860 /gene="Sand"

Query Match	3.78;	Score 72.4;	DB 5;	Length 39410;
Best Local Similarity	77.28;	Pred. No. 3.5e-09;		
Matches	88;	Conservative	0;	Mismatches 26;
			Indels	0;
			Gaps	0

QY	112	ATCCCTACCTCTCTCTGACCTATCTCTCGCATTTTGGATGACACACCCCGTACGTG	171
QY	8533	ATGCGCTATTCGAGACAGTGCACAAATTTGTTCCGATTTTTCGATCTCCACAGAGATGTT	8534
Db	172	GCTCCATCCACTGTGSCACACTTTTTCATCTTCGCAATGCCATATCCAGTGATT	225
QY	8533	GCACCATCCACTCTCGGACACACTTTTCACACATGATGGTTATCCAGTTGTT	8480
Db	172	ATCCCTACCTCTCTCTGACCTATCTCTCGCATTTTGGATGACACACCCCGTACGTG	171

RESULT 15

LOCUS	166494	7218 bp	DNA	linear	PAT 28-DEC-1997
DEFINITION	Sequence 14 from patent US 5670367.				
ACCESSION	166494				
VERSION	166494.1	GI:2724471			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				

Unclassified.
REFERENCE 1 (bases 1 to 7218)
AUTHORS Dörner, F., Scheiflinger, F. and Falkner, F., Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES
source Location/Qualifiers
BASE COUNT 1944 a 1491 c 1486 g 1929 t 368 others
ORIGIN

Query Match 3.2%; Score 64; DB 6; Length 7218;
Best Local Similarity 4.8%; Pred. No. 8.3e-07;
Matches 19; Conservative 228; Mismatches 153; Indels 0; Gaps 0;

QY 515 TGAATAACGATGAGTCTCTGAGCAGCGCAGATGAGCAACAAGCTCGGAGG 574
DB 1458 TAAAGAGATGAGAAATTTGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1399
QY 575 AGGCCACCGACTCAAGTCAGATGAATGAACATGGAATGACCTCTACTCAGA 634
DB 1398 RRR 1339
QY 635 GCCAGGCTTCTGAGTGAGAGATGATTCAGACATGCTGTGGACAGTCAGCGGTG 694
DB 1338 RRR 1279
QY 695 AGCAGCTGCTGTACTGCTGCTCCCTCAAGAAAGATGAGAAATCTGAAGAACCTC 754
DB 1278 RRR 1219
QY 755 GGAAGGCCACAGGGGAAGTGGCTGACAGCTTGAAGAAGATTGGTCTCTAGAGCA 814
DB 1218 RRR 1159
QY 815 AGTTGAAGACTCTCAACACTGAGCTGATGAGCCAGTGAAGTGAAGTGAAGTGA 874
DB 1158 RRR 1099
QY 875 AGACCTTACAAAGTCTGACAGCAGAGATCAAGCCTAAG 914
DB 1098 RRR 1059

RESULT 16
AF410847/c 2065 bp DNA linear VRL 20-SEP-2001
LOCUS Ovine herpesvirus 2 latency associated antigen (orf73) gene,
DEFINITION complete cds.
ACCESSION AF410847
VERSION AF410847.1 GI:15705839
KEYWORDS
SOURCE
ORGANISM Ovine herpesvirus 2.
Virus: dsDNA viruses, no RNA stage; Herpesviridae:
Gammaherpesvirinae.
REFERENCE 1 (bases 1 to 2065)
AUTHORS Coulter, L.J. and Reid, H.W.
TITLE Isolation and expression of three open reading frames (ORFs) from
JOURNAL Ovine herpesvirus 2
AUTHORS unpublished
TITLE 2 (bases 1 to 2065)
AUTHORS Coulter, L.J. and Reid, H.W.
JOURNAL Direct Submission
TITLE Submitted (15-AUG-2001) Virology, Moredun Research Institute,
Pentlands Science Park, Bush Loan, Penicuik, Midlothian EH26 0PZ,
UK
FEATURES
source Location/Qualifiers
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/organism="Ovine herpesvirus 2"
/vifion
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gene complement(63..1550)
/gene="orf73"
CDS complement(63..1550)
/gene="orf73"
/note="LANA; similar to HVS and HHV-8 Orf73"
/codon_start=1
/product="latency associated antigen"
/protein_id="AA105844.1"
/db_xref="GI:15705840"
/translation="MYLRSSTSTDEDEDCGRRRPKRPVTEGKGSGEGEGEGPG
GEGEGGVEGVEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEG
VEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEG
GEGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEG
GEGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEGPGEGEG
EE
EGEGEGEGPGEGEGPGEG
RKRLAPIMPTLKEATYSLHNTSKDIPVRSVRLNPNAPHNINIFTGMYTFV
IYNDEAVESLFOFLIDAMNPNQAGAVNISITGPPLPPLPNOQ"

BASE COUNT 351 a 684 c 303 g 727 t
ORIGIN

Query Match 2.9%; Score 57.6; DB 14; Length 2065;
Best Local Similarity 45.7%; Pred. No. 5.4e-05;
Matches 201; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

QY 490 AAGCAGAGATGCTGTCTTCCACCCGAAATAACAGATGATGCTCGAGCAGCGGAG 549
DB 1162 AAGGAGAGAACCTCGAGAGAGTAGAAGTCTCTGAGGAGAAAGAGAGACCTGGAG 1103
QY 550 GATGAGACCAAAACAGCTCGAGAGAGGCCACCGACTCAAGTGCAGATGAATAACCATG 609
DB 1102 GAGAGTAGAAGTCTCTGAGAGAGAGAGAGAGAGACTTGAAGAGAGAGAGAGACTG 1043
QY 610 GAGCAATGAGCTCTACTCTCAGAGAGCAGCTTCTGAGTGAAGAGAGATGATTCGAGAC 669
DB 1042 GAGGAGAGAGAGAGAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAC 983
QY 670 ATGGGTGGGAGACGTACGCGGTGAGACACTGGCTGTACTGCTGCTCCCTCAGAAA 729
DB 982 CTGAGAGAGAGAGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923
QY 730 GAGTATGAGATCTGAAGAGAGCTCGAAGGCCACAGAGGAGAGTGGCTGACAGATTGAG 789
DB 922 GACCTGTAGAGAGAGAGAGAGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863
QY 790 AAGCATTTGCTCTCTCTAGAGAGCAAGTGAAGACTCTCAACACTGAGCTGATCAGGCC 849
DB 862 AAGGACCTGAGAGAGAGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
QY 850 AAGTTAGAACTGAGGTAGCCAGAGAGACTTACAAAGTGTCTACCCAGAGATCAGAGC 909
DB 802 GAGAAAGTCTCTGAG 743
QY 910 CTAAAGAAAGAGTCTGATGA 929
DB 742 AAGAGAGAGAGAGAGAGAG 723

RESULT 17
AC067854/c 203984 bp DNA linear HTG 04-JAN-2002
LOCUS Homo sapiens chromosome 8 clone RP11-513H8 map 8, *** SEQUENCING IN
DEFINITION PROGRESS ***, 1 ordered pieces.
ACCESSION AC067854
VERSION AC067854.13 GI:18056699
KEYWORDS HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 203984)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

[illegible]

OY	718	TCCCTCAGAAAGAAGTATGACGAATTCGTAGAGAACGTCCGAAGGCCACAGGGGACTGCCT	777
Db	1879	GAGCAGCGACGAGCATTTTGAGAGACAGGAGCAAGATTNAGAGACGACGACCAGGACTTA	1938
OY	778	GACGAGGTTGAGGAAGGATTTGATGCTCCTTAGAGACAAGTTGAGAGATCTCACACTAG	837
Db	1939	GAGGACGACGAGCAGAGCATTTAGAGAGACAGGACGAGGATTAGAGAGCAGCAGGAG	1998
OY	838	CTGATCATCGGCCAAGTTTGAACTGAGCTCAGCCCCAGAGACTTTCAAAATGCTGAC	897
Db	1999	TTAGATGAGCAGGAGCAGAGCATTTAGAGAGACAGGACGAGGATTAGAGAGCAGGAG	2058
OY	898	GAGATCAGCAGCCCTTAGAAGAAGCTGTGATGATC	931
Db	2059	GAGTTAGAGGAGCAGGACGAGCATTTAGAGAGC	2092
RESULT	22		
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DEFINITION	AC073609	211158 bp DNA linear HTG 31-JAN-2002	
ACCESSION	AC073609	GI:16117946	
VERSION	AC073609.18	HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 211158)		
AUTHORS	Murphy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbati,J., Benton,J., Blamege,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P., Bunhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,U., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,L.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davey-carroll,l., Dederich,D.A., Delaney,K.R., Delgado,O., Den,A.L., Ding,Y., Dinh,H.H., Douthevalte,K.J., Draper,H., Dugan-rocha,S., Durbin,K.J., Earnhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,J., Howard,S., Huber,J., Huliyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jojivet,S., Jouhad,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kravtsov,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichteage,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mamhney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Milner,G., Milner-Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,S., Ogun,M., Okunnu,G., Nguyen,N., Nickerson,E., Nwokwenko,S., Ogum,M., Okwuonu,G., Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojuokkan,I., Rolfe,M., Ruiz,S., Savory,G., Scherer,S., Scott,G., Shen,H., Shooshitari,N., Siason,I., Sodereen,E., Sonake,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tameits,A., Tameits,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telldor,B., Thomas,N., Thomas,S., Usumali,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.		
TITLE	JOURNAL	Direct Submission	
REFERENCE	2 (bases 1 to 211158)	Unpublished	

AUTHORS
Worley, K.C.
Direct Submission
Submitted (27-JUN-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:12043813.

COMMENT

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center Project name: HBPY

Center clone name: RP23-518010

Summary Statistics

Sequencing vector: M13: L08821

Chemistry: Dye-terminator Big Dye: 88% of reads

Assembly program: Phrap; version 0.990329first call to

findPrapl

Consensus quality: 206544 bases at least Q40

Consensus quality: 209406 bases at least Q30

Consensus quality: 211582 bases at least Q20

Estimated insert size: 209430; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-1p estimation

Quality coverage: 6.6x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently

consists of 6 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 69093: contig of 69093 bp in length

69094 69193: gap of unknown length

69194 122186: contig of 52993 bp in length

122187 122286: gap of unknown length

122287 155591: contig of 33305 bp in length

155592 155691: gap of unknown length

155692 188568: contig of 32877 bp in length

188569 188668: gap of unknown length

188669 204180: contig of 15512 bp in length

204181 204280: gap of unknown length

204281 211158: contig of 6878 bp in length.

Location/Qualifiers

1. 211158

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RP23-518010"

BASE COUNT 67652 a 39628 c 38593 g 64781 t 504 others

ORIGIN

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Best Local Similarity 45.3%: Pred. No. 0.0041;

Matches 187; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

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788 AGAAG 847

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326 AGAAG 385

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

AUTHORS
Worley, K.C.
Direct Submission
Submitted (27-JUN-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:12043813.

COMMENT

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center Project name: HBPY

Center clone name: RP23-518010

Summary Statistics

Sequencing vector: M13: L08821

Chemistry: Dye-terminator Big Dye: 88% of reads

Assembly program: Phrap; version 0.990329first call to

findPrapl

Consensus quality: 206544 bases at least Q40

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Location/Qualifiers

1. 211158

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RP23-518010"

BASE COUNT 67652 a 39628 c 38593 g 64781 t 504 others

ORIGIN

Query Match 2.6%: Score 51.4; DB 2; Length 211158;

Best Local Similarity 45.3%: Pred. No. 0.0041;

Matches 187; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

488 ACAAGCAGAGATGCTGTTCACCTGAAAAAACAAGATGCTTCGAGCAGCGC 547

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26 AGAAG 85

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548 AGATGAGACCAACAGCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607

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206 AGAAG 265

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266 AGAAG 325

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QY	703	GCCTGTACTGCTGTCCCAAGAAAGATATGAGATCTGAAGAGCTCGAAGGCC	762	JOURNAL	Submitted (09-JUL-2001) Virology, University of Erlangen, Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen 91054, Germany
Db	1294	GTCGGGAGCCAAAGACCTGGAGCAGAGAGAGACGACTGCCAGACAGCAA	1353	REMARK	Sequence update by submitter
QY	763	ACAGGGAACTGGCTGACAGCTTGAGAGAGGA 794		COMMENT	On Jul 9, 2001 this sequence version replaced gi:2246466.
Db	1354	GAGGCCAGCTGAAGCACCCTGGAGAGACGGA 1385		FEATURES	Location/Qualifiers
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		inhibitory protein and v-cyclin genes, complete cds, and tegument			digested DNA from Kaposi's sarcoma biopsies"
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		Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			ODAIKYGANISVCNMGYFLVREYVRCMIGASGOMASSPPRCERKECHRPYEN
		Gammapherpesvirinae; Rhadinovirus.			GPFRKDKDIYENDAVHECNCGTILVPHSHACAVNNTWTSNMTCELAGKPPSVT
REFERENCE		1. (bases 29032 to 30108; 117733 to 118431)			HOYVLOGESLTYLKHOSVTEACNDGFVLEGSPTTCNATEMDPPLPKCVLEDIDPN
AUTHORS		Zhong W., Wang H., Herndler B. and Ganem D.			SNBGRHLHPNPKRGVNWFOENYEPPTKPTDPTATCNCQBPRLIPTSGFN
TITLE		Restricted expression of Kaposi sarcoma-associated herpesvirus			ETTSNTITFKOLEDEKTSQPNHTITSALTSKAGNFTKNTKNSDTHIATPSGD
JOURNAL		(human herpesvirus 8) genes in Kaposi sarcoma			DATPSISVQTPNVTNNAETPRLTSLIEGSPNSGTSSEKATASLHNSHNDQGI
MEDLINE		Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)			VYTLNKTQLPSTNKPPTNSOAKSSTKPRFETHNKTNPDAISLTSADVPQRRPPTL
REFERENCE		96270595			PIFRPPAKNNKYLEKQVLTGTLTVALTCGTLTTFHIFFR"
AUTHORS		2. (bases 17242 to 17856)			3194..6592
TITLE		Neipel, F., Albrecht, J.C., Ensser, A., Huang, Y.Q., Li, J.J.,			/note="ORF 06, major ssDNA binding protein homolog"
JOURNAL		Friedman-Kien, A.E. and Fleckenstein, B.			/codon_start=1
MEDLINE		Human herpesvirus 8 encodes a homolog of interleukin-6			/protein_id="AAB62603.1"
JOURNAL		J. Virol. 71 (1), 839-842 (1997)			/db_xref="GI:2246478"
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AUTHORS		3. (bases 123309 to 124082)			YEAUVFSPLHLGHVESDEPLNKAHKKIDATATASKLTSYHREIAVFNTHLFQ
TITLE		Li, M., Lee, H., Yoon, D.W., Albrecht, J.C., Fleckenstein, B., Neipel, F.			PTEQKGEKLECRSEHLEFSTVEQDGLKSPACPOLPCANEIFMAVITVEGF
JOURNAL		and Jung, J.U.			KRLVYGGKLVPPVPSQTPPVHIGEHQAFKPLDELDLFGPSRAOELCRFYNPISRYLH
MEDLINE		Kaposi's sarcoma-associated herpesvirus encodes a functional cyclin			DSIFMGIAQALRVKQVSVYIOASEROFOVDQYKIKVLOAKDFPCASCAGTGGSTLW
JOURNAL		J. Virol. 71 (3), 1984-1991 (1997)			IDSIVAEIGMSYGLSPIEGPDSCVLIANDPMPRENCETPPARALEVMHABALH
MEDLINE		97184528			ICQJRFANSVLYLTVRAKLPKRNORGDMNNSFYLOHGLCYLSEATYKENGASAFK
AUTHORS		4. (bases 122660 to 123226)			GVPVSAIDSSSTYLQHLAVASSFSPLRLARKVYLQFLPHKNTSOSYNNVDYVGA
TITLE		Thome, M., Schneider, P., Hofmann, K., Fickenscher, H., Meinel, E.,			ASOMCDLQGGCPAVCIINTLFYRMKDRPPLASLVKRPVYITAGVYNDLELIGN
JOURNAL		Neipel, F., Matlman, C., Burns, K., Bodmer, J.L., Schrotter, M.,			FATFEREEGKNVEDAPKTYTYWOLCONTEKTLASMGISEGDALRTLLVIDPSEVK
MEDLINE		Scatfield, C., Krammer, P.H., Peter, M.E. and Tschopp, J.			FKGISVYAEELKFLNCMIKNYNNPRENIKSVHHIIOACNVYQAPCPVPLTYLYK
JOURNAL		Viral FLICE-inhibitory proteins (FLiPs) prevent apoptosis induced			SILTVYIODICTSCMWYBODNPAVNGVISEEMIKMHQMTTKEKACDQKAITGGEL
MEDLINE		by death receptors			KTVHOSMRCDELDTDAITGMPAPARMQYRIRAKALMAPKTIKIKNRITFSSTAES
JOURNAL		Nature 386 (6624), 517-521 (1997)			IOAGEFKPASQSDSYVGGPYMKFLNALHKTLPSTKTSALYLIMKIQOTKQNPILPG
MEDLINE		97242415			VSGEHLTELCNVKASQSAFEINIVDLVDPDLTYSAKIKILSSILRAGGOTKAPLTPG
AUTHORS		5. (bases 1 to 133661)			LSCLSPVQLVAAEEAPHYLVGVLGSLSPDEYAKVAGRSVTVQSTLQOAVSTNLRK
TITLE		Neipel, F., Albrecht, J.C. and Fleckenstein, B.			PIITVPLVNNKTVSGNNTNPFHNCANLGVSGRDVNRNRPSPVFKNNVNSMLRK
JOURNAL		Cell-homologous genes in the Kaposi's sarcoma-associated			HYIMPIIDRLKRTVIGNSGFEAPAVKRSQNVLEPDNDNRLKTYVLELYKILGS
MEDLINE		rhadinovirus human herpesvirus 8: determinants of its			SCASLREEVITYLTPYAVLQGEVLSLSTVQAGAVPTABEGVASVYIODIIDDCELQF
JOURNAL		pathogenicity?			VQPEECLTIQGGOSVVEELFSPGVSPLVYGKKRKILASLSDLL"
MEDLINE		J. Virol. 71 (6), 4187-4192 (1997)			6609..8696
AUTHORS		6. (bases 1 to 133661)			/note="ORF 7, processing and transport protein homolog
TITLE		Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J.,			(ICP18.5)"
JOURNAL		Friedman-Kien, A.E. and Fleckenstein, B.			/codon_start=1
MEDLINE		Direct Submission			/protein_id="AAB62620.1"
JOURNAL		Submitted (17-MAR-1997) Virology, University of Erlangen, Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen 91054, Germany			/db_xref="GI:2246495"
REFERENCE		8. (bases 1 to 133661)			/translation="MAKLEAAVYADVSAIAMDCLLSYADPATLDTKSLATITGKFGS
AUTHORS		Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J.,			LHGTLPLRLRONAHCSGLSELLEHLENNVADALATAGVCSRLSPSEHSHLAD
		Friedman-Kien, A.E. and Fleckenstein, B.			TTCNKHRSVRFNFGWMALELKLTLINDVEIFKRLLSSVFCYIGSGALDEGEVLR

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Query Match 2.6%: Score 51: DB 14: Length 133661:

Best Local Similarity 45.3%: Pred. No. 0.0052:

Matches 186: Conservative 0: Mismatches 225: Indels 0: Gaps 0:

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 Qy 581 ACCGACTCAAGTCGACGATGAAAAACCTTGAAGCAAAATTGAGCTCTACTCCAGACGACG 640
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 Db 125369 TAGAGAGCAGGAGCAGGAGTTAGAGAGCAGCAGCAGGAGTTAGAGAGCAGC 125319
 RESULT 25
 AL589701/c 219200 bp DNA linear ROD 30-JAN-2002
 LOCUS AL589701
 DEFINITION Mouse DNA sequence from clone RP23-202F3 on chromosome 13.
 ACCESSION AL589701
 VERSION AL589701.9 GI:18476660
 KEYWORDS HTG.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 1 (bases 1 to 219200)
 AUTHORS Phillimore,B.
 TITLE Direct Submission
 JOURNAL Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humbrey@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Feb 1, 2002 this sequence version replaced gi:17384104.
 COMMENT During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em:, EMBL; Sw:,
 SWISSPROT; Tr:, TrEMBL; Wp:, WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-202F3 is
 from the RP21-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see http://www.chori.org/bacpac/home.htm
 VECTOR: pBACe3.6
 This sequence is the entire insert of clone RP23-202F3 The true
 left end of clone RP23-171015 is at 179956 in this sequence. The
 true right end of clone RP23-15386 is at 117857 in this sequence.
 Location/Qualifiers
 1. 219200
 FEATURES
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/organism="Mus musculus"
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/note="Single clone region. Sequence from clone PCR only."
29783..30099
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short insert library derived from a clone PCR. Restriction
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BASE COUNT 63635 a 46953 c 46566 g 61646 t
ORIGIN

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Query Match	2.6%	Score 50.8	DB 10	Length 219200
Best Local Similarity	44.6%	Pred. No. 0.0061		
Matches 199	Conservative	0	Mismatches 247	Indels 0
			Gaps	0

[illegible]

RESULT	26
LOCUS	AF360120
DEFINITION	AF360120 3012 bp DNA linear VRL 13-AUG-2001
ACCESSION	Human herpesvirus 8 ORF73 gene, complete cds.
VERSION	AF360120
KEYWORDS	AF360120.1 GI:13936995
SOURCE	.
ORGANISM	Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8.
REFERENCE	Human herpesvirus 8
AUTHORS	Vituses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
TITLE	1 (bases 1 to 3012)
	Garber,A.C., Shu,M.A., Hu,J. and Renne,R.
	Dna binding and modulation of gene expression by the
	latency-associated nuclear antigen of Kaposi's sarcoma-associated
	herpesvirus
JOURNAL	J. Virol. 75 (17), 7882-7892 (2001)
MEDLINE	21376412
PUBMED	11483733
REFERENCE	2 (bases 1 to 3012)
AUTHORS	Garber,A.C., Gonzalez,D.Y. and Renne,R.

TITLE Direct Submission
JOURNAL Submitted (13-MAR-2001) Molecular Biology and Microbiology, Case Western Reserve University, 2109 Adelbert Rd., Cleveland, OH 44106, USA

FEATURES	location/Qualifiers
source	1..3012
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CDS	/note="from KS long tumor" 1..3012

[illegible]

Query Match	2.6%;	Score 50.4;	DB 14;	Length 3012;
Best Local Similarity	45.3%;	Pred. No. 0.0064;		
Matches 183;	Conservative	0;	Mismatches 221;	Indels 0;
				Gaps 0;

OY	528	GAAGTTCCTGGAGGACGGGACGAGTTGAGACCAACCAAGCTCGGAGAGAGCCACCCAGCT	587
Db	1572	GCACAGCAGAGATTAGCAGCAGCAGCAGATGTAACACAGGACBACBAGBAGBACBAGGACA	1631
OY	588	CAAGTCAGAGATGAATAACCATGAGACAAATTGAGCTCTACTTCACAGCCAGCCTTCTGA	647
Db	1632	GCAGAGAGAGCAGGAGGACGACGAGGAGGACGAGACGAGAGTTTAGAGGACGAGGACAGGA	1691
OY	648	GGTGGAGGAGATGATTGAGACATGGGTGTGGACACAGTCAGCGGTGGAGCAGCTGGCTGT	707
Db	1692	GTTAAGAGAGCAGGAGCAGGAGGTTAGGAGGACGAGGACBAGGAATTAGAGGACBAGGACA	1751
OY	708	GTAAGCGCTGTCCCTCAAGAAAGAGTATGAGATTCGAAGGAAGCTCGGAGGCCACAGG	767
Db	1752	GGAGTTTAGAGGACGACGAGGACGAGAGTTAGAGGACGACGAGCAGAGATTGAGGAGCAGGA	1811
OY	768	GGAACTGGCTGACAGGTTTGAAGAGATTTGGTGTCTCTTAGGAGCAGCACTTGAAGACTCT	827
Db	1812	GCAGGAGTTTAGAGGAGCGAGGAGCGAGGAGTTTAGAGGACGAGGACBAGGAATTAGAGGAGA	1872
OY	828	CAACACTGAGCTGGATCAGGCCAAGTTAGAACTGAGSTCAGCCAGAGAGACTTTCAAAG	887
Db	1872	GGAGCAGAGAGTTTAGAGGAGCGCGAGGAGCTTAGAGGAGACBAGGACBAGGAGTTTAGAGA	1931
OY	888	TGCTGACCGAGAGATCAAGAGCCCAAGAAAGAACTGATGATC	931
Db	1932	GCAGGAGCAGGAGTTAGAGGACGACGAGGACGAGAGTTTAGAGGAGC	1975

RESULT	27		
AC007461/c			
LOCUS			
DEFINITION	Homo sapiens chromosome 17, clone 84_E_24, complete sequence.		

ACCESSION AC007461
VERSION AC007461.8 GI:4996920
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 180385)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone 84_E_24
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 180385)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
Hagos,B., Hatford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
Karatas,A., Lehoczkzy,D., Lieu,C., Locke,K., MacDonald,P.,
Marquis,N., McEwan,P., McGuirk,A., McKernan,K., McLaughlin,J.,
Meldrum,J., Molla,M., Morris,M., Morrow,J., Mychaleckyj,J.,
Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
Testaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-1999) Whitehead Institute/MIT Center for Genome
REFERENCE Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS 3 (bases 1 to 180385)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
Hagos,B., Hatford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
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Marquis,N., McEwan,P., McGuirk,A., McKernan,K., McLaughlin,J.,
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Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
Testaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-1999) Whitehead Institute/MIT Center for Genome
COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 4, 1999 this sequence version replaced gi:4966400.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
FEATURES
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location/Qualifiers
/organism="Homo sapiens"
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/map="17"
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/clone_lib="Alan Buckler -- per comm"
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complement(2985..3103)
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5648..5674
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5812..6020
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6303..6611
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11752..11914
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12320..12347
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20956..21137
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21830..21872
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21957..22257
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complement(22438..22538)
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Matches 196; Conservative	0; Mismatches 243; Indels 0; Gaps 0		
Db	491 AGCGAGAGTCTGTGTTCCACCGTGAATAAAGATGAATTCTCGAGCAGCGGCAGG	550	
Db	38515 AGGAAGAGAGAGGAGGGAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	38456	
Db	551 ATGACCAACAAACACTGGGAGAGGCCCAACGACTCAAGTGCAGAGATGAATCAACATGG	610	
Db	38455 AGAAG	38396	
Db	611 AGCAATTGAGCTCTACTCCAGAGCCAGCGCTTCTGAGGTGGAGAGATTCAGAGACA	670	
Db	38395 AGAAG	38336	
Db	671 TGGGTGTGGGACAGTACGCGGTGGAGCAGCTGGCTGTGTACTGCGGTGTCTCCACAGAAAG	730	
Db	38335 AGAAG	38276	

QY	731	AGTATGACAATCTGAGAACACTCGGAAGGCCACAGGGGAACCTGGCTGTACAGCTTTGAAGA	790
Db	38275	AGGAGAGAGAAGAGAGAAGAAGAAGAAGAAGAAAAGAGAGAGAGAGAAGAAGAAGAAGA	38216
QY	791	AGGATTTGTGTCCCTCTGTGAGCAAGTTGAGAGACTCTCAACACTGTGAGCTGATCAGGCCA	850
Db	38215	AGGAGGAAGAGAGAGAGAGAGGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGG	38156
QY	851	AGTTAGAACTGAGTCAAGTCCAGCCAGAAAGCACTTACAAAGTGTGACCAGAGATCAGCAACC	910
Db	38155	AGGAGAGAGAGAGAGAGAGAGAGAAGAAGAAGACAGAAAGCAGAGACAGAGAAGAAGAAGAAGA	38096
QY	911	TAAAGAAAGACAGCTGATCA	929
Db	38095	AGAAGAAGAAGAAGAAGAAGA	38077
RESULT	28		
LOCUS	AF429315	125020 bp	DNA linear PRI 18-JAN-2002
DEFINITION	Homo sapiens junctophilin 3 (JPH3) gene, partial cds.		
ACCESSION	AF429315		
VERSION	AF429315.1	GI:17646244	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 125020)		
AUTHORS	Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.		
TITLE	A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2		
JOURNAL	Nat. Genet. 29 (4), 377-378 (2001)		
MEDLINE	21583737		
PUBMED	11694876		
REFERENCE	2 (bases 1 to 125020)		
AUTHORS	Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.		
TITLE	Direct Submision		
JOURNAL	Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA		
FEATURES	Location/Qualifiers		
Source	1..125020		
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	/db_xref="GI:17646245"		
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BASE COUNT	29056 a 32731 c 30696 g 28283 t	4254 others	
ORIGIN			


```

OY      816 GTTGAGACTCTTCACACACTGAGCTGGATCGGCCCAAGTTAAGCAGAGGTCCACCAGAA 875
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DB      9611 GTTAGAGGAGCAGCAGGACCGAGGAATTAGAGGAGCAGGACGAGCAGCAAGATTAGAGAGGT 9552
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      876 GGACTTACAAGAAGTCTGACCAGGA 899
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      9551 GGAAGACGACGAGCAGGACGACGGA 9528
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT  30
AC016837          140207 bp   DNA       linear    HTG_22-DEC-2001
LOCUS           Homo sapiens clone RP11-5P19, *** SEQUENCING IN PROGRESS ***, 3
DEFINITION      unordered pieces.
ACCESSION      AC016837
VERSION         AC016837.9 GI:17977430
KEYWORDS        HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       Birren,B., Linton,L., Nusbaum,C. and Lander,E.
AUTHORS         1 (bases 1 to 140207)
TITLE           Homo sapiens chromosome, clone RP11-5P19
JOURNAL         Unpublished
REFERENCE       2 (bases 1 to 140207)
AUTHORS         Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
                Baldwin,J., Barna,N., Beckwith,R., Boguski,M., Boulikas,A.,
                Brown,A., Castle,A., Colangelo,M., Collins,S., Collumore,A.,
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                Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
COMMENT         Direct Submission
                Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Genome
                Research, 320 Charles Street, Cambridge, MA 02141, USA
                On Dec 22, 2001 this sequence version replaced gi:16874892.
                All records were identified using RepeatMasker:
                Smit, A.F.A. & Green, P. (1996-1997)
                http://ftp.genome.washington.edu/RM/RepeatMasker.html
                ----- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIRB
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
                ----- Project Information
                Center project name: U2545
                Center clone name: 5_P_19
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                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 3 contigs. The true order of the pieces
                * is not known and their order in this sequence record is
                * arbitrary. Gaps between the contigs are represented as
                * runs of N, but the exact sizes of the gaps are unknown.
                * This record will be updated with the finished sequence
                * as soon as it is available and the accession number will
                * be preserved.
                *
                * 1 3960: contig of 3960 bp in length
                * 3961 4060: gap of 100 bp
                * 4061 87705: contig of 83645 bp in length
                * 87706 87805: gap of 100 bp
                * 87806 140207: contig of 52402 bp in length.
                * Location/Qualifiers
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FEATURES
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ORIGIN

Query Match      2.5%; Score 49.2; DB 2; Length 140207;
Best Local Similarity 49.7%; Pred. No.0.017;
Matches 154; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

OY 536 TGGACAGCGCGAGATGAGACCAACAAAGCTTCGGAGAGAGGCCACCGACTCAAGTGCA 595
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Db 30922 TGGACAGAGTACAAAGATGAGGCCAAACACCTGATAGAGAGAGTGGAGACTTTGGAGGGA 30982

OY 536 AGATGAAAAACCATGAGACCAATTTGAGCTCTACTCCAGACCGAGCTTCTGAGGTGAGG 655
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Db 30983 AGCTCCAAATCCAAAGGTGGAACCAACACAGGCTTGATGTCCTGTGAGCAAGAACAAAGT 31042

OY 656 AGATATTTGAGACATATGGGTGTGGAGACATCAGCGGTGGAGACAGCTGTGTGT---ACT 712
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Db 31043 AGAGGCTCCAGAGGACGAGACGAGGCTCCGAGACAGAGAGAGTGGAGAGTGTGCGGAGG 31102

OY 713 GCGTCTCCCTCAAGAAAGAGTATGAGAAATCTTAAGAAAGCTGGAAGGCCACAGGGGAAAC 772
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Db 31103 AGGAGAGACTGTGTGATGACCAAAATGAGAGGCTTCGGGAGCAGCAGAAAGACCTACGGGAGC 31162

OY 773 TGGCTGACAGGTTTGAAGAGGATTTTGTTGCTCTCTAGAGAGCAAGTTGAAGACTCTCAACA 832
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Db 31163 AGGGTGAGAGCGCTGGGAAAGCAGGAGAGAGAGGCTATGCAAGCAGAGAGAGAGAGCTGCGGAA 31222

OY 833 CTGAGCTGCA 842
      ||||| |||||
Db 31223 AGGAGAGGGA 31232

RESULT 31
LOCUS      AC019294/c 164310 bp DNA linear PRI 02-JAN-2002
DEFINITION Homo sapiens chromosome , clone RP11-24M17, complete sequence.
ACCESSION  AC019294
VERSION     AC019294.7 GI:17998615
KEYWORDS   HRC.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 164310)
AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE     Homo sapiens chromosome, clone RP11-24M17
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 164310)
AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
            Boguslavsky,L., Boukhalter,B., Brown,A., Burdette,G., Castle,A.,
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            Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
            Zlimer,A. and Zody,M.
            Direct Submission
JOURNAL   Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            3 (bases 1 to 164310)
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Best Local Similarity 49.7%: Pred. No. 0.017;
Matches 154; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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QY 536 TGGAGCAGCGGAGATGACCAACAAGCTCGGAGAGAGCCACCGACTCAAGTCA 595
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Db 87074 TGGAGCAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 87015

QY 596 AGATGAACCATGAGCAAAATGAGCTCTACTCTCAAGACCGAGCTTCTGAGGTGAGG 655
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Db 87014 AGCTCCAACTCCAGAGTGAACCAACACGAGCTTGAAGTCTCTGAGCAAGCAAAAGT 86955

QY 656 AGATGATTCGAGACATGGGTGGGAGAGTCAAGCGGTGAGAGAGCTGCTGNT---ACT 712
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Db 86954 AGAGGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 86895

QY 713 GCGTGTCCTCAAGAAAGATGAGATCTGAAGAGAGCTCGAAGGCCACAGGGGAGAC 772
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Db 86894 AGGAGAGAGCTGTGAGCAAAATGAGAGCTTCGGAGAGAGAGAGAGAGAGAGAG 86835

QY 773 TGGCTGACAGGTGAAGAGAGATTTGGTGTCTCTAGAGAGAGAGTGAAGACTCTCAACA 832
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QY 833 CTGAGCTGGA 842
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RESULT 32
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LOCUS Homo sapiens chromosome 15 clone RP11-326L17 map 15, *** SEQUENCING
DEFINITION IN PROGRESS ***, 2 ordered pieces.
ACCESSION AC027104
VERSION AC027104.5 GI:13489207
KEYWORDS HTG: HTGS_PHASE2; HTGS_FUILLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 180795)
JOURNAL Bliren,B., Linton,L., Nusbaum,C. and Lander,E.
REFERENCE 2 (bases 1 to 180795)
        Homo sapiens chromosome 15, clone RP11-326L17

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AUTHORS Bliren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
        Anderson,S., Baldwin,D., Barna,N., Bastien,V., Beda,F.,
        Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
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Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,D., Tirrell,A., Travers,M., Triggillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (26-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2001 this sequence version replaced gi:13374714.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8783
Center clone name: 326_L17
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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* 62901 63000: gap of 100 bp
* 63001 180795: contig of 11795 bp in length.
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BASE COUNT 55798 a 38910 c 35406 g 50501 t 180 others
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Query Match      2.5%: Score 49.2; DB 2; Length 180795;
Best Local Similarity 49.7%: Pred. No. 0.018;
Matches 154; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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QY 536 TGGAGCAGCGGAGATGACCAACAAGCTCGGAGAGAGCCACCGACTCAAGTCA 595
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Db 175486 TGGAGCAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 175427

QY 596 AGATGAACCATGAGCAAAATGAGCTCTACTCTCAAGACCGAGCTTCTGAGGTGAGG 655
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DEFINITION	Mus musculus chromosome 12 clone RP23-32J01 strain C57Bl/6J,	linear	HTG 17-AUG-2001
ACCESSION	AC073564	WORKING DRAFT SEQUENCE.	12 unordered pieces.
VERSION	AC073564.3	GI:15208561	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVERFIN.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 227605)		
JOURNAL	Smith,D.R.		
REFERENCE	Genome Therapeutics Corporation Sequencing Center: Mouse Genome		
AUTHORS	Sequence Data		
TITLE	unpublished		
JOURNAL	2 (bases 1 to 227605)		
COMMENT	Smith,D.R.		
	Direct Submission		
	Submitted (24-JUN-2000) Genome Therapeutics Corporation, 100 Beaver		
	Street, Waltham, MA 02453, USA		
	On Aug 17, 2001 this sequence version replaced gi:13992669.		

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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Best Local Similarity	44.5%:	Pred. No. 0.018; Mismatches 243; Indels 0; Gaps 0
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